



TECH CENTER 1600/2300

1600

RAW SEQUENCE LISTING

DATE: 04/02/2003

PATENT APPLICATION: US/09/826,212A

TIME: 13:22:30

14

Input Set : A:\1488.1280006 Seq Lstg.txt

Output Set: N:\CRF4\04022003\I826212A.raw

5 <110> APPLICANT: Wei, Ying-Fei
 7 Yu, Guo-Liang
 9 Gentz, Reiner
 11 Ruben, Steven
 15 <120> TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
 19 <130> FILE REFERENCE: 1488.1280006
 21 <140> CURRENT APPLICATION NUMBER: 09/826,212A
 22 <141> CURRENT FILING DATE: 2001-04-05
 24 <150> PRIOR APPLICATION NUMBER: 09/006,353
 25 <151> PRIOR FILING DATE: 1998-01-13
 27 <150> PRIOR APPLICATION NUMBER: 60/054,885
 28 <151> PRIOR FILING DATE: 1997-08-07
 30 <150> PRIOR APPLICATION NUMBER: 60/035,496
 31 <151> PRIOR FILING DATE: 1997-01-14
 34 <160> NUMBER OF SEQ ID NOS: 26
 38 <170> SOFTWARE: PatentIn version 3.0
 42 <210> SEQ ID NO: 1
 44 <211> LENGTH: 1392
 46 <212> TYPE: DNA
 48 <213> ORGANISM: Homo sapiens
 52 <220> FEATURE:
 54 <221> NAME/KEY: CDS
 56 <222> LOCATION: (183)..(959)
 60 <220> FEATURE:
 62 <221> NAME/KEY: mat_peptide
 64 <222> LOCATION: (261)..()
 68 <220> FEATURE:
 70 <221> NAME/KEY: sig_peptide
 72 <222> LOCATION: (183)..(260)
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 77 cctctccacg cgcacgaact cagccaacga tttctgatag atttttggga gtttgaccag 60
 79 agatgcaagg ggtgaaggag cgcttcctac cgtagggaa ctctggggac agagcgcccc 120
 81 ggccgcctga tggccgaggc aggtgacgac ccaggacca ggacggcgtc gggaaccata 180
 83 cc atg gcc cgg atc ccc aag acc cta aag ttc gtc gtc gtc atc gtc 227
 84 Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Ile Val
 85 -25 -20 -15
 87 gcg gtc ctg ctg cca gtc cta gct tac tct gcc acc act gcc cgg cag 275
 88 Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln
 89 -10 -5 -1 1 5
 91 gag gaa gtt ccc cag cag aca gtg gcc cca cag caa cag agg cac agc 323
 92 Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser
 93 10 15 20
 95 ttc aag ggg gag gag tgt cca gca gga tct cat aga tca gaa cat act 371

ENTERED

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96 Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr
97          25          30          35
99 gga gcc tgt aac ccg tgc aca gag ggt gtg gat tac acc aac gct tcc      419
100 Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser
101          40          45          50
103 aac aat gaa cct tct tgc ttc cca tgt aca gtt tgt aaa tca gat caa      467
104 Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln
105          55          60          65
107 aaa cat aaa agt tcc tgc acc atg acc aga gac aca gtg tgt cag tgt      515
108 Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln Cys
109 70          75          80          85
111 aaa gaa ggc acc ttc cgg aat gaa aac tcc cca gag atg tgc cgg aag      563
112 Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys Arg Lys
113          90          95          100
115 tgt agc agg tgc cct agt ggg gaa gtc caa gtc agt aat tgt acg tcc      611
116 Cys Ser Arg Cys Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser
117          105          110          115
119 tgg gat gat atc cag tgt gtt gaa gaa ttt ggt gcc aat gcc act gtg      659
120 Trp Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala Thr Val
121          120          125          130
123 gaa acc cca gct gct gaa gag aca atg aac acc agc ccg ggg act cct      707
124 Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr Pro
125          135          140          145
127 gcc cca gct gct gaa gag aca atg aac acc agc cca ggg act cct gcc      755
128 Ala Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala
129 150          155          160          165
131 cca gct gct gaa gag aca atg acc acc agc ccg ggg act cct gcc cca      803
132 Pro Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro
133          170          175          180
135 gct gct gaa gag aca atg acc acc agc ccg ggg act cct gcc cca gct      851
136 Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala
137          185          190          195
139 gct gaa gag aca atg acc acc agc ccg ggg act cct gcc tct tct cat      899
140 Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His
141          200          205          210
143 tac ctc tca tgc acc atc gta ggg atc ata gtt cta att gtg ctt ctg      947
144 Tyr Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val Leu Leu
145          215          220          225
147 att gtg ttt gtt tgaagactt cactgtggaa gaaattcctt ccttacctga      999
148 Ile Val Phe Val
149 230
151 aaggttcagg taggcgctgg ctgagggcgg ggggcgctgg acactctctg ccctgcctcc      1059
153 ctctgctgtg ttccacaga cagaaacgcc tgccctgcc ccaagtccctg gtgtctccag      1119
155 cctggctcta tcttctcct tgtgatcgtc ccatcccccac atcccgtgca cccccagga      1179
157 ccctggtctc atcagtcctt ctctggagc tgggggtcca cacatctccc agccaagtcc      1239
159 aagaggcagg gccagttcct cccatcttca ggcccagcca ggcagggggc agtcggctcc      1299
161 tcaactgggt gacaaggggt aggatgagaa gtggtcacgg gatttattca gccttggtca      1359
163 gagcagaaca cagagatttt ccgtgaaaaa aaa      1392
166 <210> SEQ ID NO: 2

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Input Set : A:\1488.1280006 Seq Lstg.txt

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168 <211> LENGTH: 259
170 <212> TYPE: PRT
172 <213> ORGANISM: Homo sapiens
176 <400> SEQUENCE: 2
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179 -25 -20 -15
182 Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu
183 -10 -5 -1 1 5
186 Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe
187 10 15 20
190 Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly
191 25 30 35
194 Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
195 40 45 50
198 Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln Lys
199 55 60 65 70
202 His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln Cys Lys
203 75 80 85
206 Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys Arg Lys Cys
207 90 95 100
210 Ser Arg Cys Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp
211 105 110 115
214 Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala Thr Val Glu
215 120 125 130
218 Thr Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala
219 135 140 145 150
222 Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro
223 155 160 165
226 Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala
227 170 175 180
230 Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala
231 185 190 195
234 Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His Tyr
235 200 205 210
238 Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val Leu Leu Ile
239 215 220 225 230
242 Val Phe Val
246 <210> SEQ ID NO: 3
248 <211> LENGTH: 455
250 <212> TYPE: PRT
252 <213> ORGANISM: Homo sapiens
256 <400> SEQUENCE: 3
258 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
259 1 5 10 15
261 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
262 20 25 30
264 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
265 35 40 45
267 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys

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Input Set : A:\1488.1280006 Seq Lstg.txt

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268	50				55				60							
270	Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys	Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp
271	65					70				75					80	
273	Cys	Arg	Glu	Cys	Glu	Ser	Gly	Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu
274					85					90					95	
276	Arg	His	Cys	Leu	Ser	Cys	Ser	Lys	Cys	Arg	Lys	Glu	Met	Gly	Gln	Val
277				100					105					110		
279	Glu	Ile	Ser	Ser	Cys	Thr	Val	Asp	Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg
280			115					120					125			
282	Lys	Asn	Gln	Tyr	Arg	His	Tyr	Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe
283		130					135					140				
285	Asn	Cys	Ser	Leu	Cys	Leu	Asn	Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu
286	145					150				155					160	
288	Lys	Gln	Asn	Thr	Val	Cys	Thr	Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu
289				165				170						175		
291	Asn	Glu	Cys	Val	Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr
292			180					185					190			
294	Lys	Leu	Cys	Leu	Pro	Gln	Ile	Glu	Asn	Val	Lys	Gly	Thr	Glu	Asp	Ser
295		195					200					205				
297	Gly	Thr	Thr	Val	Leu	Leu	Pro	Leu	Val	Ile	Phe	Phe	Gly	Leu	Cys	Leu
298		210				215					220					
300	Leu	Ser	Leu	Leu	Phe	Ile	Gly	Leu	Met	Tyr	Arg	Tyr	Gln	Arg	Trp	Lys
301	225					230				235					240	
303	Ser	Lys	Leu	Tyr	Ser	Ile	Val	Cys	Gly	Lys	Ser	Thr	Pro	Glu	Lys	Glu
304			245					250					255			
306	Gly	Glu	Leu	Glu	Gly	Thr	Thr	Thr	Lys	Pro	Leu	Ala	Pro	Asn	Pro	Ser
307			260				265					270				
309	Phe	Ser	Pro	Thr	Pro	Gly	Phe	Thr	Pro	Thr	Leu	Gly	Phe	Ser	Pro	Val
310		275				280					285					
312	Pro	Ser	Ser	Thr	Phe	Thr	Ser	Ser	Ser	Thr	Tyr	Thr	Pro	Gly	Asp	Cys
313		290				295				300						
315	Pro	Asn	Phe	Ala	Ala	Pro	Arg	Arg	Glu	Val	Ala	Pro	Pro	Tyr	Gln	Gly
316	305				310				315						320	
318	Ala	Asp	Pro	Ile	Leu	Ala	Thr	Ala	Leu	Ala	Ser	Asp	Pro	Ile	Pro	Asn
319			325				330					335				
321	Pro	Leu	Gln	Lys	Trp	Glu	Asp	Ser	Ala	His	Lys	Pro	Gln	Ser	Leu	Asp
322			340				345					350				
324	Thr	Asp	Asp	Pro	Ala	Thr	Leu	Tyr	Ala	Val	Val	Glu	Asn	Val	Pro	Pro
325		355				360					365					
327	Leu	Arg	Trp	Lys	Glu	Phe	Val	Arg	Arg	Leu	Gly	Leu	Ser	Asp	His	Glu
328		370				375				380						
330	Ile	Asp	Arg	Leu	Glu	Leu	Gln	Asn	Gly	Arg	Cys	Leu	Arg	Glu	Ala	Gln
331	385				390				395						400	
333	Tyr	Ser	Met	Leu	Ala	Thr	Trp	Arg	Arg	Arg	Thr	Pro	Arg	Arg	Glu	Ala
334			405				410					415				
336	Thr	Leu	Glu	Leu	Leu	Gly	Arg	Val	Leu	Arg	Asp	Met	Asp	Leu	Leu	Gly
337			420				425				430					
339	Cys	Leu	Glu	Asp	Ile	Glu	Glu	Ala	Leu	Cys	Gly	Pro	Ala	Ala	Leu	Pro
340			435				440					445				

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Input Set : A:\1488.1280006 Seq Lstg.txt

Output Set: N:\CRF4\04022003\I826212A.raw

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342 Pro Ala Pro Ser Leu Leu Arg
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345 <210> SEQ ID NO: 4
347 <211> LENGTH: 461
349 <212> TYPE: PRT
351 <213> ORGANISM: Homo sapiens
355 <400> SEQUENCE: 4
357 Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
358 1      5      10      15
360 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
361      20      25      30
363 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
364      35      40      45
366 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
367      50      55      60
369 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
370 65      70      75      80
372 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
373      85      90      95
375 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
376      100     105     110
378 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
379      115     120     125
381 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
382      130     135     140
384 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
385 145     150     155     160
387 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
388      165     170     175
390 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
391      180     185     190
393 Asn Ala Ser Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
394      195     200     205
396 Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
397      210     215     220
399 Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
400 225     230     235     240
402 Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
403      245     250     255
405 Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
406      260     265     270
408 Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
409      275     280     285
411 Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
412      290     295     300
414 Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
415 305     310     315     320
417 Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
418      325     330     335

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:15; N Pos. 11,125,126,296,305,308,312,326,345,358,380,387,391,393,415

Seq#:15; N Pos. 425,434,438,446,458,474,478,487,489,496,499,503

Seq#:16; N Pos. 41,301,302,314,317,326

Seq#:17; N Pos. 54,55,59,62,72,134,172,181,235,269,282,308,309,338

Seq#:18; N Pos. 13,34,78,82,84,197,204,218,220,226